

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 05:08:40 ; Search time 37 Seconds
(without alignments) 405.324 Million cell updates/sec

Title: US-09-867-958-1

Perfect score: 849

Sequence: 1 MAQHARTLWYDRPMVTFME.....PPAMDIDDDSDSADATSN 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: PIR:*
2: PIR:*
3: PIR:*
4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	347.5	40.9	160 2 A56211	progesterone recep
2	346.5	40.8	160 2 B56211	progesterone recep
3	125.5	14.8	186 2 T39220	cell cycle regulat
4	121	14.3	252 2 T01305	hypothetical prote
5	114	13.4	175 2 T27543	hypothetical prote
6	99	11.7	216 2 S27382	hypothetical prote
7	91.5	10.8	704 2 A26125	heat shock protein
8	90	10.6	549 2 S37914	MZF2 protein - yea
9	89.5	10.5	484 4 A32761	hypothetical Alzhe
10	89.5	10.5	695 1 A49795	Alzheimer's diseas
11	89.5	10.5	770 1 ORH044	Alzheimer's diseas
12	88	10.4	408 2 C96502	hypothetical prote
13	88	10.4	848 2 E95092	aminopeptidase N
14	88	10.4	848 2 B97960	membrane alanyl am
15	84.5	10.0	396 2 T40559	hypothetical colle
16	83.5	9.8	685 2 A27485	Alzheimer's diseas
17	82.5	9.7	389 2 T00972	probable serpin (I
18	82	9.7	839 2 C97250	preprotein translo
19	81.5	9.6	1430 2 T27924	hypothetical prote
20	81	9.5	683 2 T21810	hypothetical prote
21	81	9.5	686 2 T21808	hypothetical prote
22	80.5	9.5	703 2 S08119	heat shock protein
23	80.5	9.5	703 2 A44983	heat shock protein
24	80	9.4	382 2 T37836	probable protein f
25	80	9.4	420 1 S22418	caldesquestrin prec
26	80	9.4	512 2 A55206	sucrose/fructan hy
27	80	9.4	521 2 A40933	probable repositin
28	80	9.4	810 2 H88565	protein ZK632.1 (I
29	79	9.3	695 2 S00550	Alzheimer's diseas

30	77	9.1	2285 2 T12796	probable transglyc
31	76.5	9.0	353 2 T07805	alternative oxidas
32	76	9.0	417 2 T22024	glucosylated prote
33	76	9.0	423 2 B72403	glucose-1-phosphat
34	76	9.0	2212 2 T28157	erythrocyte membra
35	75.5	8.9	747 2 JH0773	Alzheimer's diseas
36	75	8.8	798 2 S62791	probable lipoprote
37	75	8.8	827 2 T40394	conserved hypothet
38	75	8.8	1223 2 E88451	protein K10D2.1 (I
39	74.5	8.8	225 2 A83854	hypothetical prote
40	74.5	8.8	500 2 S50508	ANP1 protein - yea
41	74.5	8.8	700 2 S57415	Hsp83 protein - Ye
42	74	8.7	267 2 A40269	cyclin C - fruit f
43	74	8.7	409 1 J01396	caldesquestrin prec
44	74	8.7	459 2 T21097	hypothetical prote
45	74	8.7	482 2 S34275	protein disulfide-

ALIGNMENTS

RESULT 1

A56211
progesterone receptor-related protein p23 - human
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000
C:Accession: A56211
R:Johnson, J.L.; Belto, T.G.; Krco, C.J.; Toft, D.O.
Mol. Cell. Biol. 14, 1956-1963, 1994
A:Title: Characterization of a novel 23-kilodalton protein of inactive progesterone
A:Reference number: A56211; MUID:94158868; PMID:8114727
A:Accession: A56211
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-160 <JOB>
A:Cross-references: GB:L24804; GB:L24805; NID:9438651; PIDN:AAA18537.1; PID:9438652
C:Genetics:
A:Gene: GDB:PGRP
A:Cross-references: GDB:337371
C:Superfamily: Caenorhabditis elegans hypothetical protein ZC395.10
C:Keywords: steroid hormone receptor

Query Match 40.9%; Score 347.5; DB 2; Length 160;
Best Local Similarity 43.4%; Pred. No. 5.8e-25;
Matches 66; Conservative 30; Mismatches 53; Indels 3; Gaps 2;

QY 4 QHARTLWYDRPMVTFMEFCVEDSTDVHVLIEDHRTVESC-KNADGVELYNEIFYAKVNS 62
DB 2 QPASAKWYDRDRDYVIEFCVEDSKDVNVNFEKSKLTFSCLGSDNFKHLNIEDLPHCIDP 61
QY 63 KDSODKRSRSITCFVRKKEKVPRLTKEDIKRVNLSVDFDNMRMDEGDEMLAHE 122
DB 62 NDSKHKRTDRSILCLCRGSGSQSWPRLTKERAKNWLVSDFNNKWDWEDSDSDMSND 121
QY 123 HYAEILKKVSTKRP--PAMDIDDDSDSADD 152
DB 122 RFSEMMNMGGDEVDYDLEFVYGADDDSDSD 153

RESULT 2

B56211
progesterone receptor-related protein p23 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000
C:Accession: B56211
R:Johnson, J.L.; Belto, T.G.; Krco, C.J.; Toft, D.O.
Mol. Cell. Biol. 14, 1956-1963, 1994
A:Title: Characterization of a novel 23-kilodalton protein of inactive progesterone
A:Reference number: A56211; MUID:94158868; PMID:8114727
A:Accession: B56211
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-160 <JOB>

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117; PMID:1905108
 A:Accession: A49795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <PDB>
 A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing

Query Match 10.5%; Score 89.5; DB 1; Length 695;
 Best Local Similarity 22.2%; Pred. No. 2.3;
 Matches 30; Conservative 25; Mismatches 43; Indels 37; Gaps 4;

QY 17 VMEPCVEVDSTVYHLEIDHRIYFSCNAGCVELNIEFYAKNSKSDQDKRSRITC 76
 DB 153 VAKETSEKSTNHH---DYGMLIPC---GIDKFRGEVFCPCPLAESDNDVSDAD--- 201
 QY 77 EVKMKKEKVAWPRITKEDIKPWLISVDFDWMRDGDEEELAHVEHYAELLKVTSTRP 136
 DB 202 -----EEDSDVWVGADPTDYADGSEDKYVEAEVEAEVEE----- 239
 QY 137 PPMADLDDSDSDAD 151
 DB 240 ---EEADDEDED 250

RESULT 11
 ORH004
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIIa inhibi
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 protein precursor splice form APP(770)

C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #ext_change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A3260; A35486; I39452; I39453; I59562; A44
 4668; A28583; A29302; A60805; JLO0037; A50121; A60355; A50111; A38384; S29076; S38252; S3
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The P16A4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427; PMID:2783775
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13466 (695)
 A>Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA1830.1; PID:g871360
 A>Note: alternative splice form APP(695)
 R:Faust, F.; Labiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
 A:Reference number: A32277; MUID:8915870; PMID:2538123
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AA13654.1; PID:g516074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1246-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
 A:Reference number: A33260; MUID:89392030; PMID:2675837
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:g178663; PIDN:AA51768.1; PID:g178665
 R:Prelli, F.; Levy, E.; van Dineen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of

A:Reference number: A35486; MUID:90321244; PMID:2196878
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A>Note: 693-Gln was found in DNA isolated from HCMVA-D patients
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318; PMID:2110105
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB,
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:g178613; PIDN:AA59502.1; PID:g178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB,
 A:Molecule type: DNA
 A:Residues: 1-530, 'OMLMPVPAFWEAKYGR' <YOS2>
 A:Cross-references: GB:M34875; NID:g178608; PIDN:AA59501.1; PID:g178615
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168; PMID:1908403
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van D
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hem
 A:Reference number: I39453; MUID:90260663; PMID:2111584
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:g178618; PIDN:AA51727.1; PID:g178620
 A>Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzh
 A:Reference number: I59562; MUID:92022553; PMID:1925564
 A:Accession: I59562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AA51991.1; PID:g236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wiseman, E.M.; Alonso, M.E.; Palst, S.M.; Ander
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindr for
 A:Reference number: A44017; MUID:93035397; PMID:1415269
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <RAM1>
 A:Cross-references: GB:S45135; NID:g257377; PIDN:AA523645.1; PID:g257378
 A:Experimental source: familial Alzheimer disease family SB
 A>Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <RAM2>
 A:Cross-references: GB:S45136; NID:g257379; PIDN:AA523646.1; PID:g257380
 A:Experimental source: familial Alzheimer disease family LT
 A>Note: sequence extracted from NCBI backbone (NCBIP:115376)
 A>Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-su
 A:Reference number: A03134; MUID:87144572; PMID:2881207
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:I00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A>Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascul

A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:q178539; PIDN:AAA51722.1; PID:q178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldhaber, D.; Lemman, M.T.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:q178706; PIDN:AAA35540.1; PID:q178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ken
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15532; NID:q177957; PIDN:AAA51564.1; PID:q177958
R:Dyck, T.; Weldemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pred
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Porte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitor
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:Q28816; PIDN:CAA30041.1; PID:g929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three f
A:Reference number: A30320
A:Accession: A30320
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A:Status: not compared with conceptual translation

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A:Molecule type: mRNA
A:Residues: 606-770 <YIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid CDNA derived from mRNA of the Alzheimer disease
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M8734; NID:g178572; PIDN:AA51726.1; PID:g178573
A>Note: The authors translated the codon GAA for residue 599 as Gly, ACC for residue
B as Val, GGG for residue 609 as Asp, AAT for residue 610 as Gly, and GGT for residu
A>Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther

Query Match      10.5%; Score 89.5; DB 1; Length 770;
Best Local Similarity 22.2%; Pred. No. 2.6;
Matches 30; Conservative 25; Mismatches 43; Indels 37; Gaps 4;

Oy 17 VFMEECEDSTVHVLIEDHRIVECKKNADGYELNYEIEFYAVANKSDOKRSRSITC 76
    | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |
Db 153 VAKETCSKSTUHL-----DYGMLIPC-----GIDKKFGVEHVCCPLAESNVDSADR--- 201
                                ||| ||||
Oy 77 FVRKKRYKRVAMPRLTKEDIKPYLWLVDFPNMRDMEGDEEMLAHEHYALLKKVSTRP 136
                                ||| ||||
Db 202 -----EEDSDSVWMGGADPTDYADGSDSKVYEVAEEAEVEAVEE----- 239
                                ||| ||||
Oy .137 PRAMDDLUDDSAD 151
    : | | | | |
Db 240 ----BEADDDEDDED 250

RESULT 12
C96502
[hypothetical protein F28H19.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: C96502
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alic
Chih, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hutzar, L.
ature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kin
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maitl, R.; Martz
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talli
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96502
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-408 <STO>
A:Cross-references: GB:AE005173; NID:g7523665; PIDN:AAF63105.1; GSPDB:GN00141
C:Genetics:
A:Gene: F28H19.9
A:Map position: 1
C:Superfamily: Arabidopsis hypothetical protein F7N22.18

Query Match      10.4%; Score 88; DB 2; Length 408;
Best Local Similarity 20.7%; Pred. No. 1.7;
Matches 41; Conservative 25; Mismatches 50; Indels 82; Gaps 9;

Oy 8 TLWDPRMYVMEECEDSTVHVLIEDHRIVF-----SCKNADG-----V 48
    | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |
Db 65 TLWFD-----DDSTDAARY----RIIFEDIKEPHANMSQTSKATIDOWYTEPA 109
                                ||| ||||
Oy 49 ELTV-----ELIEFYAKNSKDSODKRSRSITCVRRKKRKVAMPRLTKEDIKPVW 99
    : | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |
Db 110 QVYWMDSSINKRVAYEEBAKLKS-----RMSDOVSRRKGNNKK-----GDEAKPKW 156
    : | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |
Oy 100 LSYDFDN-----WRDWBGDEEMELAHEHYVELLLKVS-----T 133
    : | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |

```

Db 157 IDPVSXGLVGFQMDPPSEKRYTAAEMDMMIRAKASINTVQARPHTKLVQENGVRLE 216
QY 134 KRPPAMPDDDDSDAD 151
| : : : : :
Db 217 KKTPELLELDETHRRAD 234

RESULT 13

aminopeptidase N [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: E95092
R:Reichlin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Held
on, J.D.; Hickey, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Umayam, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357205; PMID:11463916
A:Accession: E95092
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-848 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK74934.1; PID:914972273; GSPDB:GN00164; TIGR:SP4
A:Experimental source: Strain TIGR4
C:Genetics:
A:Gene: SP0797
C:Superfamily: membrane alanyl aminopeptidase

Query Match 10.4%; Score 88; DB 2; Length 848;
Best Local Similarity 21.1%; Pred. No. 4;
Matches 41; Conservative 19; Mismatches 60; Indels 74; Gaps 7;

QY 9 LMYRPMYVMEF-CVE-----DSTD---VHYLIE----- 34
| : : : : :
Db 311 LMLNESFANMMEYCVDTIEPSWNIFFDQGVPLALERDXTDGVSVHVEKHPDEIN 370
| : : : : :
QY 35 ---DHRIYFS-----CKNADGVELYNEIEFYAKVNSKDSOD---KRSSRS 73
| : : : : :
Db 371 TLFGAIVYAAKGRMLMHLRMGLDADPAKGLHAFKHOXSNTIGSLMDALGQASGRD 430
| : : : : :
QY 74 ITCFVRKMKKEVAMPRLT-----KEDIKPVWLSVDFPNWRMEGDE 114
| : : : : :
Db 431 VAAFDMSWLEOPGVPLTVKVENVDLAKISOKOFIGENEDKRLMVPLNSNMKGLPDTL 490
| : : : : :
QY 115 EMELAHVEHYAELL 128
| : : : : :
Db 491 ETESEIPIGYAALL 504

RESULT 14

membrane alanyl aminopeptidase (EC 3.4.11.2) [imported] - Streptococcus pneumoniae (stre
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 01-Feb-2002
C:Accession: B97960
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
r, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B97960
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-848 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99510.1; PID:915458296; GSPDB:GN00174
C:Genetics:
A:Gene: pepN
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase

Query Match 10.4%; Score 88; DB 2; Length 848;
Best Local Similarity 21.1%; Pred. No. 4;
Matches 41; Conservative 19; Mismatches 60; Indels 74; Gaps 7;

QY 9 LMYRPMYVMEF-CVE-----DSTD---VHYLIE----- 34
| : : : : :
Db 311 LMLNESFANMMEYCVDTIEPSWNIFFDQGVPLALERDXTDGVSVHVEKHPDEIN 370
| : : : : :
QY 35 ---DHRIYFS-----CKNADGVELYNEIEFYAKVNSKDSOD---KRSSRS 73
| : : : : :
Db 371 TLFGAIVYAAKGRMLMHLRMGLDADPAKGLHAFKHOXSNTIGSLMDALGQASGRD 430
| : : : : :
QY 74 ITCFVRKMKKEVAMPRLT-----KEDIKPVWLSVDFPNWRMEGDE 114
| : : : : :
Db 431 VAAFDMSWLEOPGVPLTVKVENVDLAKISOKOFIGENEDKRLMVPLNSNMKGLPDTL 490
| : : : : :
QY 115 EMELAHVEHYAELL 128
| : : : : :
Db 491 ETESEIPIGYAALL 504

RESULT 15

hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40559
R:Lyne, M.H.; Rajadream, M.A.; Barrell, B.G.; Xiang, Z.; Hunt, I.C.; Aves, S.J.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21936
A:Accession: T40559
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-396 <LYN>
A:Cross-references: EMBL:AL110506; PIDN:CA854823.1; GSPDB:GN00067
A:Experimental source: strain 972h-; cosmid c577
C:Genetics:
A:Gene: SPAC577.15c
A:Map position: 2

Query Match 10.0%; Score 84.5; DB 2; Length 396;
Best Local Similarity 25.8%; Pred. No 3.4;
Matches 34; Conservative 25; Mismatches 58; Indels 15; Gaps 4;

QY 26 STDVAVLIEDHRIYFSCKNADGVELYNEIEFYAKVNSKDSODKSSRSITCFVRKMKKEK- 84
| : : : : :
Db 184 AVDAIPDSKDEKI---RLADIYDLGLGELSLTEINFQASQDLKTA-----LEWKEXV 232
| : : : : :
QY 85 --VAMPRLTKEDIKPVWLSVDFPNWRMEGDEEMELAHVEHYAELLKVKSTRPPAMPD 142
| : : : : :
Db 233 YNVSNNLTLSFAHYKIALALEFTNPED--PSNKRACEHYEKAELIKVNLNERENEVYTD 291
| : : : : :
QY 143 LDDSDSDADAT 154
| : : : : :
Db 292 KKGKQKAEST 303

Search completed: March 20, 2003, 05:21:01
Job time : 45 secs